



001560-393 5

SEQUENCE LISTING

<110> Kakimoto, Tatsuo

<120> Homoeobox Gene Encoding a Protein Involved in Differentiation

<130> 001560-393

<140> US 09/787,737

<141> 2001-03-22

<150> PCT/JP00/04904

<151> 2000-07-21

<150> JP 11-207995

<151> 1999-07-22

<160> 8

<170> PatentIn version 3.0

<210> 1

<211> 1214

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (36)..(1010)

<223> Nucleotide sequence coding for a protein involved in differentiation

<400> 1

ctttagctct cgattatcat cattacacca tcatc atg tcc tcc tca aac aaa 53

Met Ser Ser Ser Asn Lys

1 5

aat tgg cca agc atg ttc aaa tcc aaa cct tgc aac aat aat cat cat 101

Asn Trp Pro Ser Met Phe Lys Ser Lys Pro Cys Asn Asn Asn His His

10 15 20

cat caa cat gaa atc gat act cca tct tac atg cac tac tct aat tgc 149

His Gln His Glu Ile Asp Thr Pro Ser Tyr Met His Tyr Ser Asn Cys

25 30 35

aac cta tca tct tcc ttt tcc tca gat cgg ata cca gat cct aaa ccg 197

Asn Leu Ser Ser Ser Phe Ser Ser Asp Arg Ile Pro Asp Pro Lys Pro

40 45 50

aga tgg aat cct aaa ccg gag cag att agg ata ctc gaa tca atc ttc 245

Arg Trp Asn Pro Lys Pro Glu Gln Ile Arg Ile Leu Glu Ser Ile Phe

55 60 65 70

aat tcc ggt act att aac cca cct aga gag gag att caa aga atc cgg 293

Asn Ser Gly Thr Ile Asn Pro Pro Arg Glu Glu Ile Gln Arg Ile Arg	
75 80 85	
atc cgg ctt caa gaa tat ggt caa atc ggt gac gca aac gtg ttt tac	341
Ile Arg Leu Gln Glu Tyr Gly Gln Ile Gly Asp Ala Asn Val Phe Tyr	
90 95 100	
tgg ttt caa aac cgg aaa tct cga gca aaa cac aag ctt cgt gtt cat	389
Trp Phe Gln Asn Arg Lys Ser Arg Ala Lys His Lys Leu Arg Val His	
105 110 115	
cac aaa agc cct aaa atg tca aag aag gac aag acg gtt att cct agt	437
His Lys Ser Pro Lys Met Ser Lys Lys Asp Lys Thr Val Ile Pro Ser	
120 125 130	
act gac gct gat cat tgt ttt ggt ttt gtt aac caa gaa acc gga tta	485
Thr Asp Ala Asp His Cys Phe Gly Phe Val Asn Gln Glu Thr Gly Leu	
135 140 145 150	
tat ccg gtt caa aac aat gag ttg gtg gta acc gaa ccg gcc ggt ttt	533
Tyr Pro Val Gln Asn Asn Glu Leu Val Val Thr Glu Pro Ala Gly Phe	
155 160 165	
cta ttt ccg gtt cat aat gat ccg agc gct gct caa tca gcg ttt ggt	581
Leu Phe Pro Val His Asn Asp Pro Ser Ala Ala Gln Ser Ala Phe Gly	
170 175 180	
ttt ggc gat ttt gtt gta ccg gtg gta acg gaa gaa ggg atg gca ttc	629
Phe Gly Asp Phe Val Val Pro Val Val Thr Glu Glu Gly Met Ala Phe	
185 190 195	
tct acc gtt aat aac ggc gtt aat ttg gag act aac gaa aat ttt gat	677
Ser Thr Val Asn Asn Gly Val Asn Leu Glu Thr Asn Glu Asn Phe Asp	
200 205 210	
aaa att ccg gcg atc aat tta tac ggc gga gat gga aat ggc ggt gga	725
Lys Ile Pro Ala Ile Asn Leu Tyr Gly Gly Asp Gly Asn Gly Gly Gly	
215 220 225 230	
aat tgt ttt cct cct ttg act gtt cca tta acc atc aat caa tct caa	773
Asn Cys Phe Pro Pro Leu Thr Val Pro Leu Thr Ile Asn Gln Ser Gln	
235 240 245	
gaa aaa cga gat gta gga tta tcc ggt ggt gaa gac gtc gga gat aat	821
Glu Lys Arg Asp Val Gly Leu Ser Gly Gly Glu Asp Val Gly Asp Asn	
250 255 260	
gtt tat ccg gtg aga atg acg gtg ttt att aac gag atg cct atc gaa	869
Val Tyr Pro Val Arg Met Thr Val Phe Ile Asn Glu Met Pro Ile Glu	
265 270 275	
gta gtg tct gga tta ttc aac gtt aag gca gct ttc gga aac gat gcc	917
Val Val Ser Gly Leu Phe Asn Val Lys Ala Ala Phe Gly Asn Asp Ala	
280 285 290	
gtt ttg atc aac tcg ttt ggc cag cct att ctt aca gat gaa ttt ggt	965
Val Leu Ile Asn Ser Phe Gly Gln Pro Ile Leu Thr Asp Glu Phe Gly	

```

295          300          305          310
gtt act tat caa cct ctc caa aat ggc gca atc tat tat ctt att      1010
Val Thr Tyr Gln Pro Leu Gln Asn Gly Ala Ile Tyr Tyr Leu Ile
          315          320          325

tagaagatat tgaaaagcaa atgttatggt gctatggata aatattaata taataataaa 1070
agatttctgc gatttattta gttattaatt agataagaat ttcatttctt atctttttaa 1130
tttatgaaca atttacagga catttacatt ttcgagactt tgaaaaataa agaatgaaat 1190
taagttaaaa aaaaaaaaaa aaaa      1214

```

```

<210> 2
<211> 325
<212> PRT
<213> Arabidopsis thaliana

```

```

<220>
<223> Amino acid sequence coding for a protein involved in
      differentiation

```

```

<400> 2

```

```

Met Ser Ser Ser Asn Lys Asn Trp Pro Ser Met Phe Lys Ser Lys Pro
1          5          10          15

```

```

Cys Asn Asn Asn His His His Gln His Glu Ile Asp Thr Pro Ser Tyr
20          25          30

```

```

Met His Tyr Ser Asn Cys Asn Leu Ser Ser Ser Phe Ser Ser Asp Arg
35          40          45

```

```

Ile Pro Asp Pro Lys Pro Arg Trp Asn Pro Lys Pro Glu Gln Ile Arg
50          55          60

```

```

Ile Leu Glu Ser Ile Phe Asn Ser Gly Thr Ile Asn Pro Pro Arg Glu
65          70          75          80

```

```

Glu Ile Gln Arg Ile Arg Ile Arg Leu Gln Glu Tyr Gly Gln Ile Gly
85          90          95

```

```

Asp Ala Asn Val Phe Tyr Trp Phe Gln Asn Arg Lys Ser Arg Ala Lys
100          105          110

```

```

His Lys Leu Arg Val His His Lys Ser Pro Lys Met Ser Lys Lys Asp
115          120          125

```

Lys Thr Val Ile Pro Ser Thr Asp Ala Asp His Cys Phe Gly Phe Val  
130 135 140

Asn Gln Glu Thr Gly Leu Tyr Pro Val Gln Asn Asn Glu Leu Val Val  
145 150 155 160

Thr Glu Pro Ala Gly Phe Leu Phe Pro Val His Asn Asp Pro Ser Ala  
165 170 175

Ala Gln Ser Ala Phe Gly Phe Gly Asp Phe Val Val Pro Val Val Thr  
180 185 190

Glu Glu Gly Met Ala Phe Ser Thr Val Asn Asn Gly Val Asn Leu Glu  
195 200 205

Thr Asn Glu Asn Phe Asp Lys Ile Pro Ala Ile Asn Leu Tyr Gly Gly  
210 215 220

Asp Gly Asn Gly Gly Gly Asn Cys Phe Pro Pro Leu Thr Val Pro Leu  
225 230 235 240

Thr Ile Asn Gln Ser Gln Glu Lys Arg Asp Val Gly Leu Ser Gly Gly  
245 250 255

Glu Asp Val Gly Asp Asn Val Tyr Pro Val Arg Met Thr Val Phe Ile  
260 265 270

Asn Glu Met Pro Ile Glu Val Val Ser Gly Leu Phe Asn Val Lys Ala  
275 280 285

Ala Phe Gly Asn Asp Ala Val Leu Ile Asn Ser Phe Gly Gln Pro Ile  
290 295 300

Leu Thr Asp Glu Phe Gly Val Thr Tyr Gln Pro Leu Gln Asn Gly Ala  
305 310 315 320

Ile Tyr Tyr Leu Ile  
325

<210> 3  
<211> 1518  
<212> DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (152)..(1285)

&lt;223&gt; Nucleotide sequence coding for a protein involved in differentiation

&lt;400&gt; 3

```

tttttattta tcttttcttt agccattctg ttccctgtct cttcctcttc tctttttgac      60
acatcacatc atcatcacat catcattcaa catcaatcat catcatatgc atacacatac      120
atctgtgttc tgcggatcga gttaattagt t atg gct tct tcg aat aga cac      172
                               Met Ala Ser Ser Asn Arg His
                               1                               5

tgg cca agc atg ttc aag tcc aaa cct cat ccc cat caa tgg caa cat      220
Trp Pro Ser Met Phe Lys Ser Lys Pro His Pro His Gln Trp Gln His
                               10                               15                               20

gac atc aac tct cct ctc ttg cct tct gct tct cac cga tct tct cct      268
Asp Ile Asn Ser Pro Leu Leu Pro Ser Ala Ser His Arg Ser Ser Pro
                               25                               30                               35

ttc tct tca gga tgt gaa gtg gag agg agt cca gag cca aaa cca aga      316
Phe Ser Ser Gly Cys Glu Val Glu Arg Ser Pro Glu Pro Lys Pro Arg
40                               45                               50                               55

tgg aat cca aag cca gag cag att cgg ata ctt gaa gca atc ttt aac      364
Trp Asn Pro Lys Pro Glu Gln Ile Arg Ile Leu Glu Ala Ile Phe Asn
                               60                               65                               70

tcc ggg atg gtg aat cct cca aga gag gag atc agg agg att agg gct      412
Ser Gly Met Val Asn Pro Pro Arg Glu Glu Ile Arg Arg Ile Arg Ala
                               75                               80                               85

cag ctt caa gaa tac ggc caa gtc ggt gat gct aac gtc ttc tac tgg      460
Gln Leu Gln Glu Tyr Gly Gln Val Gly Asp Ala Asn Val Phe Tyr Trp
90                               95                               100

ttc caa aac cgt aag tcc cgt agt aaa cac aaa ctc cgc ctc ctc cac      508
Phe Gln Asn Arg Lys Ser Arg Ser Lys His Lys Leu Arg Leu Leu His
105                               110                               115

aac cac tcc aaa cac tct ctc cct caa acg caa ccg cag ccg cag ccg      556
Asn His Ser Lys His Ser Leu Pro Gln Thr Gln Pro Gln Pro Gln Pro
120                               125                               130                               135

caa cct tcg gct tcc tct tcc tct tcc tcc tcc tct tcc tcc tcc aaa      604
Gln Pro Ser Ala Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Lys
                               140                               145                               150

tcc acc aaa ccc cga aaa agc aag aac aag aac aac act aat ctc tct      652
Ser Thr Lys Pro Arg Lys Ser Lys Asn Lys Asn Asn Thr Asn Leu Ser
                               155                               160                               165

```

ttg ggt ggt agt caa atg atg ggg atg ttt cca ccg gaa ccg gcg ttt Leu Gly Gly Ser Gln Met Met Gly Met Phe Pro Pro Glu Pro Ala Phe 170 175 180	700
ctc ttc ccg gtc tcc act gtc gga ggg ttt gaa ggt atc acc gtc tca Leu Phe Pro Val Ser Thr Val Gly Gly Phe Glu Gly Ile Thr Val Ser 185 190 195	748
tcc caa tta ggg ttt ctc tcc ggt gat atg att gag caa caa aaa ccg Ser Gln Leu Gly Phe Leu Ser Gly Asp Met Ile Glu Gln Gln Lys Pro 200 205 210 215	796
gct cca acg tgt acc gga ctc ctg ctg agt gag atc atg aac ggt agt Ala Pro Thr Cys Thr Gly Leu Leu Leu Ser Glu Ile Met Asn Gly Ser 220 225 230	844
gtg agt tat gga act cat cat caa caa cac ttg agt gag aaa gaa gtt Val Ser Tyr Gly Thr His His Gln Gln His Leu Ser Glu Lys Glu Val 235 240 245	892
gaa gaa atg agg atg aag atg ttg caa cag cca cag act cag att tgt Glu Glu Met Arg Met Lys Met Leu Gln Gln Pro Gln Thr Gln Ile Cys 250 255 260	940
tac gct acc act aat cat caa ata gct tct tac aac aac aac aac aac Tyr Ala Thr Thr Asn His Gln Ile Ala Ser Tyr Asn Asn Asn Asn Asn 265 270 275	988
aac aat aac atc atg ctt cat att cct ccc act act tct act gcc acc Asn Asn Asn Ile Met Leu His Ile Pro Pro Thr Thr Ser Thr Ala Thr 280 285 290 295	1036
act att act act tcg cat tct ctc gct act gtc cca tca act tcg gac Thr Ile Thr Thr Ser His Ser Leu Ala Thr Val Pro Ser Thr Ser Asp 300 305 310	1084
cag ctt caa gtt caa gcg gac gca cga ata aga gtt ttc atc aat gaa Gln Leu Gln Val Gln Ala Asp Ala Arg Ile Arg Val Phe Ile Asn Glu 315 320 325	1132
atg gag ctt gaa gtg agc tca gga ccg ttc aat gtg agg gat gca ttt Met Glu Leu Glu Val Ser Ser Gly Pro Phe Asn Val Arg Asp Ala Phe 330 335 340	1180
ggg gaa gag gtt gtt ctg att aat tcc gcg ggt cag ccc att gtc acc Gly Glu Glu Val Val Leu Ile Asn Ser Ala Gly Gln Pro Ile Val Thr 345 350 355	1228
gat gaa tat ggc gtc gct ctt cac cct ctt caa cac gga gcc tcg tac Asp Glu Tyr Gly Val Ala Leu His Pro Leu Gln His Gly Ala Ser Tyr 360 365 370 375	1276
tat ctg atc tagtcgtgtg ggagatttga gtttgaagaa gaaattaaga Tyr Leu Ile	1325
cctgtctctt tctttcacca tctactcgta cgtaggctta aatgttaaga ttttataaag	1385

tattggtttc agttacctgt tgtgacggtg tttatgtatg agtttcggac aacattcaca 1445  
 aaactctctc gttaaattgt tgacctaata atatatgatg tgtgtttcat tattaataaaa 1505  
 aaaaaaaaaa aaa 1518

<210> 4  
 <211> 378  
 <212> PRT  
 <213> Arabidopsis thaliana

<220>

<223> Amino acid sequence coding for a protein involved in differentiation

<400> 4

Met Ala Ser Ser Asn Arg His Trp Pro Ser Met Phe Lys Ser Lys Pro  
 1 5 10 15

His Pro His Gln Trp Gln His Asp Ile Asn Ser Pro Leu Leu Pro Ser  
 20 25 30

Ala Ser His Arg Ser Ser Pro Phe Ser Ser Gly Cys Glu Val Glu Arg  
 35 40 45

Ser Pro Glu Pro Lys Pro Arg Trp Asn Pro Lys Pro Glu Gln Ile Arg  
 50 55 60

Ile Leu Glu Ala Ile Phe Asn Ser Gly Met Val Asn Pro Pro Arg Glu  
 65 70 75 80

Glu Ile Arg Arg Ile Arg Ala Gln Leu Gln Glu Tyr Gly Gln Val Gly  
 85 90 95

Asp Ala Asn Val Phe Tyr Trp Phe Gln Asn Arg Lys Ser Arg Ser Lys  
 100 105 110

His Lys Leu Arg Leu Leu His Asn His Ser Lys His Ser Leu Pro Gln  
 115 120 125

Thr Gln Pro Gln Pro Gln Pro Gln Pro Ser Ala Ser Ser Ser Ser  
 130 135 140

Ser Ser Ser Ser Ser Ser Lys Ser Thr Lys Pro Arg Lys Ser Lys Asn

100



<210> 5  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Primer.

<400> 5  
gaagatctca tcatgtcctc ctcaaac

27

<210> 6  
<211> 30  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Primer.

<400> 6  
cggagctcta aataagataa tagattgcgc

30

<210> 7  
<211> 32  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Primer.

<400> 7  
gctctagaac aatggcttct tcgaatagac ac

32

<210> 8  
<211> 32  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> Primer.

<400> 8  
tcccccgggc tgatcagata gtacgaggct cc

32